



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/710,262
Source: 1600
Date Processed by STIC: 4/30/02

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebs/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
Or
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
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Revised 01/29/2002

TECH CENTER 1600/2900

MAY 08 2002

RECEIVED

#6
1652

RECEIVED

MAY 08 2002

1600

Raw Sequence Listing Error Summary

TECH CENTER 1600/2900

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 091710,262

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics
Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 ☐ Invalid Line Length
The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 ☒ Misaligned Amino
Numbering
The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 ☐ Non-ASCII
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 ☐ Variable Length
Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 ☐ PatentIn 2.0
"bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 ☐ Skipped Sequences
(OLD RULES)
Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 ☐ Skipped Sequences
(NEW RULES)
Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 ☐ Use of n's or Xaa's
(NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 ☐ Invalid <213>
Response
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 ☐ Use of <220>
Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 ☐ PatentIn 2.0
"bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 ☐ Misuse of n
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.



Does Not Comply
Corrected Diskette Needed

1600

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/710,262

DATE: 04/30/2002
TIME: 15:45:19

Input Set : A:\EP.txt
Output Set: N:\CRF3\04302002\I710262.raw

3 <110> APPLICANT: Rosenberg, Eugene
4 Ron, Elisha
5 Orr, Elisha
6 Paitan, Yossi
8 <120> TITLE OF INVENTION: GENE CLUSTER
10 <130> FILE REFERENCE: 2290.00101
12 <140> CURRENT APPLICATION NUMBER: 09/710,262
13 <141> CURRENT FILING DATE: 2000-11-10
15 <160> NUMBER OF SEQ ID NOS: 20
17 <170> SOFTWARE: PatentIn Ver. 2.1

*Sample pages of
misalignment of amino acid numbering
throughout. See error summary
sheet item 3.*

ERRORED SEQUENCES

19 <210> SEQ ID NO: 1
20 <211> LENGTH: 2392
21 <212> TYPE: DNA
22 <213> ORGANISM: Myxococcus xanthus
24 <400> SEQUENCE: 1
25 Val Asp Pro Ala Arg Leu Thr Arg Ala Trp Glu Gly Leu Leu Glu Arg
W--> 26 1 5 10
E--> 27 15
29 Tyr Pro Leu Leu Ala Gly Ala Ile Arg Val Glu Gly Thr Glu Pro Val
W--> 30 20 25
E--> 31 30
33 Ile Val Pro Ser Gly Gln Val Ser Ala Glu Val His Glu Val Pro Ser
W--> 34 35 40 45
36 Val Ser Asp Ser Ala Leu Val Ala Thr Leu Arg Ala Ser Ala Lys Val
W--> 37 50 55 60
39 Pro Phe Asp Leu Ala Cys Gly Pro Leu Ala Arg Leu His Leu Tyr Ser
W--> 40 65 70 75
E--> 41 80
43 Arg Ser Glu His Glu His Val Leu Leu Leu Cys Phe His His Leu Val
W--> 44 85 90
E--> 45 95
47 Leu Asp Gly Ala Ser Val Ala Pro Leu Leu Asp Ala Leu Arg Glu Arg
W--> 48 100 105
E--> 49 110
51 Tyr Ala Gly Thr Glu Ala Lys Ala Gly Leu Leu Glu Val Pro Ile Val
W--> 52 115 120 125
54 Ala Pro Tyr Arg Ala Ala Val Glu Trp Glu Gln Leu Ala Ile Gly Gly
W--> 55 130 135 140
57 Asp Glu Gly Arg Arg His Leu Asp Tyr Trp Arg His Val Leu Ala Thr

→ The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/710,262

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Input Set : A:\EP.txt

Output Set: N:\CRF3\04302002\I710262.raw

```

E--> 531 2240
      533 Ala Asp Phe Asp Pro Leu Phe Phe Asn Ile Ser Pro Arg Glu Ala Thr
W--> 534                                2245                                2250
E--> 535 2255
      537 Ser Met Asp Pro Gln Glu Arg Leu Phe Leu Gln Ser Cys Trp Glu Val
W--> 538                                2260                                2265
E--> 539 2270
      541 Leu Glu Asp Ala Gly Tyr Thr Arg Asp Ser Leu Ala Gln Arg Phe Gly
W--> 542                                2275                                2280                                2285
      544 Ser Ala Val Gly Val Phe Ala Gly Ile Thr Lys Thr Gly Tyr Glu Leu
W--> 545                                2290                                2295                                2300
      547 Tyr Gly Ala Glu Leu Glu Gly Arg Asp Ala Ser Val Arg Pro Tyr Thr
W--> 548 2305                                2310                                2315
E--> 549 2320
      551 Ser Phe Ala Ser Val Ala Asn Arg Val Ser Tyr Leu Leu Asp Leu Lys
W--> 552                                2325                                2330
E--> 553 2335
      555 Gly Pro Ser Met Pro Val Asp Thr Met Cys Ser Ala Ser Leu Thr Ala
W--> 556                                2340                                2345
E--> 557 2350
      559 Val His Met Ala Cys Glu Ala Leu Gln Arg Gly Ala Cys Val Met Ala
W--> 560                                2355                                2360                                2365
      562 Ile Ala Gly Gly Val Asn Leu Tyr Val His Pro Ser Ser Tyr Val Ser
W--> 563                                2370                                2375                                2380
      565 Leu Ser Gly Gln Gln Met Leu Ser
E--> 566 2385                                2390
      697 <210> SEQ ID NO: 3
      698 <211> LENGTH: 785
      699 <212> TYPE: DNA
      700 <213> ORGANISM: Myxococcus xanthus
      702 <400> SEQUENCE: 3
      703 Met Lys Val Val Asn Lys Leu Leu Glu Lys Leu Pro Asp Val Val Ala
W--> 704 1                                5                                10
E--> 705 15
      707 Gly Lys Val Pro Asp Val Lys Leu Gln Asp Gln Asp Ile Lys Val Pro
W--> 708                                20                                25
E--> 709 30
      711 Leu Ala Gln Gly Thr Phe Thr Glu Glu Lys Ile Leu Pro Pro Lys Leu
W--> 712                                35                                40
E--> 713 45
      715 Ala Met His Gly Phe Thr Leu Ser Phe Glu Ala Thr Gly Glu Ala Ser
W--> 716                                50                                55                                60
      718 Ile Arg Asn Phe Asn Ser Leu Gly Asp Val Asp Glu Asn Gly Ile Ile
W--> 719 65                                70                                75
E--> 720 80
      722 Gly Glu Pro Ser Pro Glu Ser Ala Glu Pro Gly Pro Arg Pro Gln Leu
W--> 723                                85                                90
E--> 724 95
      726 Leu Leu Gly Ser Asp Ile Gly Trp Met Arg Tyr Gln Val Ser Ala Arg

```

RAW SEQUENCE LISTING

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DATE: 04/30/2002

TIME: 15:45:19

Input Set : A:\EP.txt

Output Set: N:\CRF3\04302002\I710262.raw

```

W--> 862          690          695          700
      864 Met Val Arg Leu Arg Arg Ala Ile Asp Glu Arg Lys Ala Pro Asp Glu
W--> 865 705          710          715
E--> 866 720
      868 Leu Arg Thr Val Phe Gly Glu Leu Glu Gly Met Trp Thr Thr Gly Phe
W--> 869          725          730
E--> 870 735
      872 His Leu Arg Ala Ala Gly Ser Leu Leu Ser Asp Leu Ala Gln Ser Thr
W--> 873          740          745
E--> 874 750
      876 Pro Leu Gly Leu Ala Gly Val Glu Arg Thr Leu Thr Val Arg Val Ala
W--> 877          755          760          765
      879 Asp Ser Glu Glu Gln Leu Val Phe Ser Thr Ala Arg Ser Thr Gly Ala
W--> 880          770          775          780
      882 Ala
E--> 883 785
      886 <210> SEQ ID NO: 4
      887 <211> LENGTH: 529
      888 <212> TYPE: DNA
      889 <213> ORGANISM: Myxococcus xanthus
      891 <400> SEQUENCE: 4
      892 Met Pro Ser Gly Cys Tyr Gly Ala Ala Ser Ala Phe Val Leu Pro Pro
W--> 893 1          5          10
E--> 894 15
      896 Leu Pro Ala Met Pro Gln Ala Pro Ser Asp Val Ser Gln Val Leu Leu
W--> 897          20          25
E--> 898 30
      900 Pro Phe Gly Gly Leu Val Gly Arg Glu Val Asp Leu Asp Ala Phe Leu
W--> 901          35          40
E--> 902 45
      904 Gln Thr Leu Met Asp Arg Ile Ala Ile Thr Leu Gln Ala Asp Arg Gly
W--> 905          50          55          60
      907 Thr Leu Trp Leu Leu Asp Pro Ala Arg Arg Glu Leu Phe Ser Arg Ala
W--> 908 65          70          75
E--> 909 80
      911 Ala His Leu Pro Glu Val Ser Gln Ile Arg Val Lys Leu Gly Gln Gly
W--> 912          85          90
E--> 913 95
      915 Val Ala Gly Thr Val Ala Lys Ala Gly His Ala Ile Asn Val Pro Asp
W--> 916          100          105
E--> 917 110
      919 Pro Arg Gly Glu Gln Arg Phe Phe Ala Asp Ile Asp Arg Met Thr Gly
W--> 920          115          120          125
      922 Tyr Arg Thr Thr Ser Leu Leu Ala Val Pro Leu Arg Asp Gly Asp Gly
W--> 923          130          135          140
      925 Ala Leu Tyr Gly Val Leu Gln Val Leu Asn Arg Arg Gly Glu Asp Arg
W--> 926 145          150          155
E--> 927 160
      929 Phe Thr Asp Glu Asp Thr Gln Arg Leu Thr Ala Ile Ala Ser Gln Val

```

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/710,262DATE: 04/30/2002
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Input Set : A:\EP.txt

Output Set: N:\CRF3\04302002\I710262.raw

Invalid Line Length:**The rules require that a line not exceed 72 characters in length. This includes spaces.**

Seq#:1; Line(s) 26,30,34,37,40,44,48,52,55,58,62,66,74,77,81,85,89,92,95,99
Seq#:1; Line(s) 103,107,110,113,117,121,129,132,136,140,148,151,155,159,167
Seq#:1; Line(s) 170,174,178,182,185,188,192,196,200,203,206,210,214,218,221
Seq#:1; Line(s) 224,228,232,236,239,242,246,250,254,257,260,264,268,272,275
Seq#:1; Line(s) 278,282,290,293,296,300,308,311,314,318,322,326,329,332,336
Seq#:1; Line(s) 344,347,350,354,358,362,365,368,372,380,383,386,390,394,398
Seq#:1; Line(s) 401,404,408,412,416,419,422,426,430,434,437,440,444,448,452
Seq#:1; Line(s) 455,458,462,466,470,473,476,480,484,488,491,494,498,502,506
Seq#:1; Line(s) 509,512,516,520,524,527,530,534,538,542,545,548,552,560,563
Seq#:3; Line(s) 704,708,716,719,723,727,731,734,737,741,745,749,752,755,759
Seq#:3; Line(s) 763,771,774,778,782,786,789,792,796,800,804,807,810,814,818
Seq#:3; Line(s) 826,829,833,837,841,844,847,851,855,859,862,865,869,873,877
Seq#:3; Line(s) 880
Seq#:4; Line(s) 893,897,901,905,908,912,916,920,923,926,930,934,938,941,944
Seq#:4; Line(s) 948,952,960,963,967,971,979,982,986,990,994,997,1000,1004
Seq#:4; Line(s) 1008
Seq#:5; Line(s) 1026,1030,1038,1041,1045,1049,1053,1056,1059,1063,1067,1071
Seq#:5; Line(s) 1074,1077,1081,1085,1089
Seq#:6; Line(s) 1102,1106,1110,1113,1116,1120,1124,1128,1131,1134
Seq#:8; Line(s) 1170,1174,1178,1182,1185,1189,1193,1197,1200,1203,1207,1211
Seq#:8; Line(s) 1215,1218,1221,1225,1229,1233,1236,1239,1243,1247,1251,1254
Seq#:8; Line(s) 1257,1261
Seq#:9; Line(s) 1275,1279,1287,1290,1294,1298,1302,1305,1308,1312,1316,1320
Seq#:9; Line(s) 1323,1326,1330,1334,1338,1341,1344
Seq#:10; Line(s) 1358,1362,1370,1373
Seq#:11; Line(s) 1387,1391,1395,1398,1401,1405,1409,1413,1416,1419,1423
Seq#:11; Line(s) 1427,1431,1434,1437,1441,1449,1452,1455,1459,1463
Seq#:12; Line(s) 1481,1485,1489,1493,1496,1500,1504,1512,1515,1519
Seq#:13; Line(s) 1529,1533,1537,1541,1544,1548,1552,1556,1559,1562,1566
Seq#:13; Line(s) 1570,1578,1581,1585,1589,1597,1600,1604,1608,1612,1615
Seq#:13; Line(s) 1618,1622,1626,1630,1633,1636
Seq#:14; Line(s) 1646,1650,1654,1658,1661,1665,1669,1673,1676,1679,1683
Seq#:14; Line(s) 1687,1691,1694,1697,1701,1705,1709,1712,1715
Seq#:15; Line(s) 1725,1729,1737,1740,1744,1748,1752,1755,1758,1762,1766
Seq#:15; Line(s) 1770,1773,1776,1780,1784,1788,1791,1794,1798
Seq#:16; Line(s) 1808,1812,1816,1820,1823,1827,1831,1839,1842,1846,1850
Seq#:16; Line(s) 1854,1857,1860,1864,1868,1872,1875,1878,1882,1890,1893
Seq#:16; Line(s) 1896,1900
Seq#:17; Line(s) 1914,1918,1922,1925,1928,1932,1936,1940,1943,1946,1950
Seq#:17; Line(s) 1954,1962,1965,1969
Seq#:18; Line(s) 1983,1987,1991,1995,1998,2002,2006,2014,2017,2021,2025
Seq#:18; Line(s) 2029,2032,2035,2039
Seq#:19; Line(s) 2053,2057,2061,2065,2068,2072,2076,2080,2083,2086,2090

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/710,262

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Input Set : A:\EP.txt

Output Set: N:\CRF3\04302002\I710262.raw

Seq#:19; Line(s) 2094,2098,2101,2104,2108,2112,2116,2119,2122,2126,2130

Seq#:19; Line(s) 2138,2141,2145,2149

VERIFICATION SUMMARY

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Input Set : A:\EP.txt

Output Set: N:\CRF3\04302002\I710262.raw

L:26 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:27 M:254 E: No. of Bases conflict, this line has no nucleotides.
L:30 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
M:254 Repeated in SeqNo=1
L:34 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:37 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:40 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:44 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:48 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:52 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:55 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:58 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:62 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:66 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:70 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:74 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:77 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:81 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:85 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:89 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:92 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:95 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:99 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:103 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:107 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:110 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:113 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:117 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:121 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:125 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:129 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:132 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:136 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:140 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:144 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:148 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:151 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:155 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:159 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:163 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:167 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:170 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:174 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:178 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:182 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:185 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:188 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:192 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1

VERIFICATION SUMMARY

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Input Set : A:\EP.txt

Output Set: N:\CRF3\04302002\I710262.raw

L:196 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:200 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:203 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:206 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:566 M:252 E: No. of Seq. differs, <211> LENGTH:Input:2392 Found:0 SEQ:1
L:705 M:254 E: No. of Bases conflict, this line has no nucleotides.
M:254 Repeated in SeqNo=3
L:883 M:252 E: No. of Seq. differs, <211> LENGTH:Input:785 Found:0 SEQ:3
L:894 M:254 E: No. of Bases conflict, this line has no nucleotides.
M:254 Repeated in SeqNo=4
L:1015 M:252 E: No. of Seq. differs, <211> LENGTH:Input:529 Found:0 SEQ:4
L:1027 M:254 E: No. of Bases conflict, this line has no nucleotides.
M:254 Repeated in SeqNo=5
L:1092 M:252 E: No. of Seq. differs, <211> LENGTH:Input:292 Found:0 SEQ:5
L:1103 M:254 E: No. of Bases conflict, this line has no nucleotides.
M:254 Repeated in SeqNo=6
L:1138 M:252 E: No. of Seq. differs, <211> LENGTH:Input:168 Found:0 SEQ:6
L:1160 M:252 E: No. of Seq. differs, <211> LENGTH:Input:79 Found:0 SEQ:7
L:1171 M:254 E: No. of Bases conflict, this line has no nucleotides.
M:254 Repeated in SeqNo=8
L:1265 M:252 E: No. of Seq. differs, <211> LENGTH:Input:420 Found:0 SEQ:8
L:1276 M:254 E: No. of Bases conflict, this line has no nucleotides.
M:254 Repeated in SeqNo=9
L:1348 M:252 E: No. of Seq. differs, <211> LENGTH:Input:325 Found:0 SEQ:9
L:1359 M:254 E: No. of Bases conflict, this line has no nucleotides.
M:254 Repeated in SeqNo=10
L:1376 M:252 E: No. of Seq. differs, <211> LENGTH:Input:83 Found:0 SEQ:10
L:1388 M:254 E: No. of Bases conflict, this line has no nucleotides.
M:254 Repeated in SeqNo=11
L:1471 M:252 E: No. of Seq. differs, <211> LENGTH:Input:374 Found:0 SEQ:11
L:1482 M:254 E: No. of Bases conflict, this line has no nucleotides.
M:254 Repeated in SeqNo=12
L:1519 M:252 E: No. of Seq. differs, <211> LENGTH:Input:171 Found:0 SEQ:12
L:1530 M:254 E: No. of Bases conflict, this line has no nucleotides.
M:254 Repeated in SeqNo=13
L:1636 M:252 E: No. of Seq. differs, <211> LENGTH:Input:475 Found:0 SEQ:13
L:1647 M:254 E: No. of Bases conflict, this line has no nucleotides.
M:254 Repeated in SeqNo=14
L:1715 M:252 E: No. of Seq. differs, <211> LENGTH:Input:318 Found:0 SEQ:14
L:1726 M:254 E: No. of Bases conflict, this line has no nucleotides.
M:254 Repeated in SeqNo=15
L:1798 M:252 E: No. of Seq. differs, <211> LENGTH:Input:330 Found:0 SEQ:15
L:1809 M:254 E: No. of Bases conflict, this line has no nucleotides.
M:254 Repeated in SeqNo=16
L:1903 M:252 E: No. of Seq. differs, <211> LENGTH:Input:417 Found:0 SEQ:16
L:1915 M:254 E: No. of Bases conflict, this line has no nucleotides.
M:254 Repeated in SeqNo=17
L:1973 M:252 E: No. of Seq. differs, <211> LENGTH:Input:262 Found:0 SEQ:17
L:1984 M:254 E: No. of Bases conflict, this line has no nucleotides.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/710,262

DATE: 04/30/2002

TIME: 15:45:20

Input Set : A:\EP.txt

Output Set: N:\CRF3\04302002\I710262.raw

M:254 Repeated in SeqNo=18

L:2040 M:252 E: No. of Seq. differs, <211> LENGTH:Input:256 Found:0 SEQ:18

L:2054 M:254 E: No. of Bases conflict, this line has no nucleotides.

M:254 Repeated in SeqNo=19

L:2149 M:252 E: No. of Seq. differs, <211> LENGTH:Input:424 Found:0 SEQ:19